

Pinus mugo cover showed a strong indication that *Apodemus flavicollis* preferred a habitat dominated by *P. mugo*. However, the raw data show that no used trap was located within the dwarf pine cover (neither trap point had negative values of distance to the nearest *P. mugo* patch). This would characterize the habitat of occurrence of *A. flavicollis* as the edge of *P. mugo* stands. The typical habitat of *Apodemus flavicollis* is described as open mature forests, preferably deciduous with open ground level. Its occurrence at ecotones, grasslands or shrubby habitat is considered atypical (NIETHAMMER 1978; GURNELL 1985). Yet, the ecotone of dwarf pine and subalpine meadows is the habitat preferred by this species in the subalpine zone in western Tatras. Here, large seeds forming the base of *A. flavicollis* diet (NIETHAMMER 1978; SMETTAN 1996) are in short supply as well as in coniferous forests in general. These are usually considered suboptimal habitats or serving as corridors (ANGELSTAM et al. 1987; KOTZAGEORGIS and MASON 1996; ŠMAHA 1996). Since the locality does not enable individuals to remain through the winter, but their survival is possible during the vegetation season, it could be considered a suboptimal habitat for this species (GLIWICZ 1989, 1993). However, sporadic occurrence of *A. flavicollis* at the locality indicates that the species is not a regular seasonal resident to this area. This assumption is supported also by the fact that the sexual ratio is deviant from the expected values, which occurs in dispersers (GLIWICZ 1988), i. e., most individuals were present at the locality exclusively in a single trapping series and by low

number of captures per individual. In a habitat in which reproduction per individual is low, population density has a tendency to decline (GAINES et al. 1994) and the population shows a high turnover rate (MAZURKIEWICZ 1991, 1994) in this type of habitat, is referred to as a "sink" habitat. This is the case for the area investigated in the present study.

The appearance of yellow-necked mice can be explained by high population densities in altitudes below the research area. *Apodemus flavicollis* tends to occur in "nuclei" within occupied forests, which are relatively stable centers of occurrence, and spatially oscillate depending on the population density (GURNELL 1985). If we assume a positive correlation between population density in a given nucleus and the effort that the dispersers make to travel from the nucleus (distance \times number of dispersers), then population density at our study plots indicates the culmination phases at lower altitudes. A crowded habitat would force subdominant individuals to seek vacant space and they will appear at our study plots. If such a situation occurs, the population probably exhibits a three year cycle.

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Short communication

Non-invasive PCR sexing of rabbits (*Oryctolagus cuniculus*) and hares (*Lepus europaeus*)

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Genetic sex verification has important implications for population studies of free-ranging animals relying on the knowledge of reproductive status and sex ratio of the animals. In the brown hare (*Lepus euroaeus*) a continuous population decline has been reported in many European countries (FLUX and ANGERMANN 1990). The reason for the decrease is under debate (McLAREN et al. 1997; PANEK and KAMIENIARZ 1999; REYNOLDS and TAPPER 1995), and population studies of this species are therefore highly needed. The collection of blood causes stress due to trapping and handling of animals (JESSUP 1993) that could affect the parameters under investigation, particularly in a highly irritable species like the brown hare. Previous studies have demonstrated the potential for faeces collected in the field as a suitable source of DNA for genotyping and sexing free-ranging mammals (TABERLET et al. 1997). Since no sex-specific DNA sequences are known for the brown hare, we initially developed a PCR test for sex determination in rabbits (*Oryctolagus cuniculus*) and adapted it for sexing hares (*Lepus europaeus*). The assay co-amplifies a part of the Y-chromosomal Sry and the autosomal rabbit transferrin gene, which is used as an internal amplification control.

Because most sex-identification methods are not species specific, some precautions

have to be made to be aware of possible contamination with extraneous DNA, especially when animal remains such as hair or faeces are used as source for DNA analysis (TABERLET et al. 1997). In contrast to this universal primer approach, primers described in this report are placed in rabbit-specific sequence regions. To test the specificity of the assay, we amplified DNA from human, mouse, horse, and sheep, but none of these species amplified even under low stringency conditions (data not shown).

We first verified the accuracy of the assay by analysing genomic DNA from a total of 78 rabbits. Genomic DNA was isolated from 200 µl EDTA-blood from 24 adult males and 27 females of different rabbit breeds (GEMMELL and AKIYAMA 1996). For 27 new born rabbits, buccal swabs sampled with Q-Tips were used for sexing in order to apply a minimal invasive technique. The cut cotton-wool end of the Q-tip was placed in a 1.5 ml vial containing 600 µl digestion buffer (GEMMELL and AKIYAMA 1996) and stored at room temperature. Genomic DNA was obtained as described above by digestion of the whole swab with proteinase K (80 µg) for 2 hours at 56 °C. DNA was then extracted from the supernatant (GEMMELL and AKIYAMA 1996). Primers (Tab. 1) amplifying a fragment from the Sry region were designed accord-